

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lee, Jong Y.
- (ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN
RECEPTOR PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C.
 - (B) STREET: 120 Sixth South Street, Suite 2500
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/106,815
 - (B) FILING DATE: 16-AUG-1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ellinger, Mark S.
 - (B) REGISTRATION NUMBER: 34,812
 - (C) REFERENCE/DOCKET NUMBER: 07004/002002
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612/335-5070
 - (B) TELEFAX: 612/288-9696

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: BamH1 linker at 5' end
followed by sequence for amino acids 25 through 29 of the full
length human EpoR protein. Forward primer for Sequence ID No. 2.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

00016159.013098

TTGGATCC GCG CCC CCG CCT AAC
Ala Pro Pro Pro Asn
1 5

23

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: EcoRI linker followed by sequence complementary to coding sequence for amino acids 226 through 222 of full length human EpoR protein. Reverse primer for Sequence ID No. 1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAATTCGGG GTCCAGGTCG CT

22

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)
- (ix) FEATURE:
 - (A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T.
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Smith, D.B.
Johnson, K.S.
 - (B) TITLE: Single-step purification of polypeptides
expressed in Escherichia coli as fusions with
glutathione-S-transferase.
 - (C) JOURNAL: Gene
 - (D) VOLUME: 67
 - (F) PAGES: 31-40

00016159.013099

THE FIFTH

CTG GTT CCG CGT GGA TCC
Leu Val Pro Arg Gly Ser
10

18

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(iv) ANTI-SENSE: NO

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Jones, S.S.
(C) JOURNAL: Blood
(D) VOLUME: 76
(E) ISSUE: 1
(F) PAGES: 31-35
(G) DATE: 1990

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Noguchi, C.T.
(C) JOURNAL: Blood
(D) VOLUME: 78
(E) ISSUE: 10
(F) PAGES: 2548-2556
(G) DATE: 1991

ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys

48

CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
25 30 35

96

CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu

40 45 50

144

GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
55 60 65 70

192

GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
75 80 85

240

TAC Tyr	CAG Gln	CTC Leu	GAG Glu 90	GAT Asp	GAG Glu	CCA Pro	TGG Trp	AAG Lys 95	CTG Leu	TGT Cys	CGC Arg	CTG Leu	CAC His 100	CAG Gln	GCT Ala	288
CCC Pro	ACG Thr	GCT Ala 105	CGT Arg	GGT Gly	GCG Ala	GTG Val	CGC Arg 110	TTC Phe	TGG Trp	TGT Cys	TCG Ser	CTG Leu 115	CCT Pro	ACA Thr	GCC Ala	336
GAC Asp	ACG Thr 120	TCG Ser	AGC Ser	TTC Phe	GTG Val 125	CCC Pro 125	CTA Leu	GAG Glu	TTG Leu	CGC Arg	GTC Val 130	ACA Thr	GCA Ala	GCC Ala	TCC Ser	384
GGC Gly 135	GCT Ala	CCG Pro	CGA Arg	TAT Tyr	CAC His 140	CGT Arg	GTC Val	ATC Ile	CAC His	ATC Ile 145	AAT Asn	GAA Glu	GTA Val	GTG Val	CTC Leu 150	432
CTA Leu	GAC Asp	GCC Ala	CCC Pro	GTG Val 155	GGG Gly	CTG Leu	GTG Val	GCG Ala	CGG Arg 160	TTG Leu	GCT Ala	GAC Asp	GAG Glu	AGC Ser 165	GGC Gly	480
CAC His	GTA Val	GTG Val	TTG Leu 170	CGC Arg	TGG Trp	CTC Leu	CCG Pro 175	CCG Pro	CCT Pro	GAG Glu	ACA Thr	CCC Pro	ATG Met 180	ACG Thr	TCT Ser	528
CAC His	ATC Ile	CGC Arg 185	TAC Tyr	GAG Glu	GTG Val	GAC Asp	GTC Val 190	TCG Ser	GCC Ala	GGC Gly	AAC Asn	GGC Gly 195	GCA Ala	GGG Gly	AGC Ser	576
GTA Val 200	CAG Gln	AGG Arg	GTG Val	GAG Glu	ATC Ile	CTG Leu 205	GAG Glu	GGC Gly	CGC Arg	ACC Thr	GAG Glu 210	TGT Cys	GTG Val	CTG Leu	AGC Ser	624
AAC Asn 215	CTG Leu	CGG Arg	GGC Gly	CGG Arg	ACG Thr 220	CGC Arg	TAC Tyr	ACC Thr	TTC Phe	GCC Ala 225	GTC Val	CGC Arg	GCG Ala	CGT Arg	ATG Met 230	672
GCT Ala	GAG Glu	CCG Pro	AGC Ser	TTC Phe 235	GGC Gly	GGC Gly	TTC Phe	TGG Trp	AGC Ser 240	GCC Ala	TGG Trp	TCG Ser	GAG Glu	CCT Pro 245	GTG Val	720
TCG Ser	CTG Leu	CTG Leu	ACG Thr 250	CCT Pro	AGC Ser	GAC Asp	CTG Leu	GAC Asp 255	CCC Pro	CTC Leu	ATC Ile	CTG Leu	ACG Thr 260	CTC Leu	TCC Ser	768
CTC Leu	ATC Ile	CTC Leu 265	GTG Val	GTC Val	ATC Ile	CTG Leu	GTG Val 270	CTG Leu	CTG Leu	ACC Thr	GTG Val	CTC Leu	GCG Ala	CTG Leu	CTC Leu	816
TCC Ser	CAC His 280	CGC Arg	CGG Arg	GCT Ala	CTG Leu	AAG Lys 285	CAG Gln	AAG Lys	ATC Ile	TGG Trp	CCT Pro 290	GGC Gly	ATC Ile	CCG Pro	AGC Ser	864
CCA Pro 295	GAG Glu	AGC Ser	GAG Glu	TTT Phe	GAA Glu 300	GGC Gly	CTC Leu	TTC Phe	ACC Thr	ACC Thr 305	CAC His	AAG Lys	GGT Gly	AAC Asn	TTC Phe 310	912
CAG Gln	CTG Leu	TGG Trp	CTG Leu	TAC Tyr 315	CAG Gln	AAT Asn	GAT Asp	GGC Gly	TGC Cys 320	CTG Leu	TGG Trp	TGG Trp	AGC Ser	CCC Pro 325	TGC Cys	960
ACC Thr	CCC Pro	TTC Phe	ACG Thr 330	GAG Glu	GAC Asp	CCA Pro	CCT Pro	GCT Ala 335	TCC Ser	CTG Leu	GAA Glu	GTC Val	CTC Leu	TCA Ser	GAG Glu	1008

CGC TGC TGG GGG ACG ATG CAG GCA GTG GAG CCG GGG ACA GAT GAT GAG	1056
Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu	
345 350 355	
GGC CCC CTG CTG GAG CCA GTG GGC AGT GAG CAT GCC CAG GAT ACC TAT	1104
Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr	
360 365 370	
CTG GTG CTG GAC AAA TGG TTG CTG CCC CGG AAC CCG CCC AGT GAG GAC	1152
Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp	
375 380 385 390	
CTC CCA GGG CCT GGT GGC AGT GTG GAC ATA GTG GCC ATG GAT GAA GGC	1200
Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly	
395 400 405	
TCA GAA GCA TCC TCC TGC TCA TCT GCT TTG GCC TCG AAG CCC AGC CCA	1248
Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro	
410 415 420	
GAG GGA GCC TCT GCT GCC AGC TTT GAG TAC ACT ATC CTG GAC CCC AGC	1296
Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser	
425 430 435	
TCC CAG CTC TTG CGT CCA TGG ACA CTG TGC CCT GAG CTG CCC CCT ACC	1344
Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr	
440 445 450	
CCA CCC CAC CTA AAG TAC CTG TAC CTT GTG GTA TCT GAC TCT GGC ATC	1392
Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile	
455 460 465 470	
TCA ACT GAC TAC AGC TCA GGG GAC TCC CAG GGA GCC CAA GGG GGC TTA	1440
Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu	
475 480 485	
TCC GAT GGC CCC TAC TCC AAC CCT TAT GAG AAC AGC CTT ATC CCA GCC	1488
Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala	
490 495 500	
GCT GAG CCT CTG CCC CCC AGC TAT GTG GCT TGC TCT T AG	1527
Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser	
505 510	

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